



SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS FOR TREATING OR
PREVENTING PNEUMOCOCCAL INFECTION

<130> 12844-002001

<140> US 10/702,305

<141> 2003-11-06

<150> US 60/424,497

<151> 2002-11-07

<160> 26

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<212> PRT

<213> Streptococcus pneumoniae

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Ile Lys Glu Gly Asn Gln Leu Pro Asp Glu Phe Val Val Ile Glu Arg
35 40 45
Lys Lys Arg Ser Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala
50 55 60
Thr Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val Asp Glu
65 70 75 80
Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala Val Asp Arg Ala Pro
85 90 95
Met Thr Tyr Ser Ile Asp Leu Pro Gly Leu Ala Ser Ser Asp Ser Phe
100 105 110
Leu Gln Val Glu Asp Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn
115 120 125
Asp Leu Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn Val
130 135 140
Pro Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His Ser Met Glu Gln
145 150 155 160
Leu Lys Val Lys Phe Gly Ser Asp Phe Glu Lys Thr Gly Asn Ser Leu
165 170 175
Asp Ile Asp Phe Asn Ser Val His Ser Gly Glu Lys Gln Ile Gln Ile
180 185 190
Val Asn Phe Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys
195 200 205
Asn Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu Asp Leu Lys
210 215 220

Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val
 225 230 235 240
 Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser
 245 250 255
 Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val
 260 265 270
 Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys
 275 280 285
 Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr
 290 295 300
 Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe
 305 310 315 320
 Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu
 325 330 335
 Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu
 340 345 350
 Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser
 355 360 365
 Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asn Glu Leu Ser Tyr
 370 375 380
 Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn
 385 390 395 400
 Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 405 410 415
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala
 420 425 430
 Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val
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gatgagtttgc	ttgttatcga	aagaaagaag	cgagactgt	cgacaaatac	180
tctgtacacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcg	240
accttggtag	agaataatcc	cacttctt	gcccgtcgat	gtgctccgat	300
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tcaagtgttc	gcggagcggt	aaacgatttgc	ttggctaagt	ggcatcaaga	420
gtcaataatg	tcccagctag	aatgcagtagt	gaaaaatca	cggtcacag	480
ctcaaggtca	agtttggttc	tgactttgaa	aagacaggga	attcttcttga	540
aactctgtcc	attcaggcga	aaagcagatt	cagattgtt	attttaagca	600
acagttagcg	tagatgtgt	taaaaatcca	ggagatgtgt	ttcaagatac	660
gaggatttaa	aacagagagg	aatttctgca	gagcgtcctt	ttcgagtgtt	720
gcttatgggc	gccaagtcta	tctcaagtttgc	gaaaccacga	gtaagagtga	780
gctgcttttgc	aagcttgc	aaaaggagtc	aaggtagctc	ctcagacaga	840
attttggaca	atacagaagt	gaaggcggtt	atttttagggg	gcgacccaaag	900
cgagttgtaa	caggcaaggt	ggatatggta	gaggacttga	ttcaagaagg	960
acagcagatc	atccaggtttc	gccgatttcc	tatacaactt	cttttttacg	1020
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ctctctgtca	aaatttagaga	gcgttccggg	ttgcctggg	aatggtggcg	1320
aaaaaaacccg	atttgcact	agtgcgttaag	cgacgattt	ctatttgggg	1380
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gatgagtttgc	ttgttatcga	aagaaagaag	cgagactgt	cgacaaatac	180
tctgtacacag	ctaccaacga	cagtcgcctc	tatcctggag	cacttctcg	240
accttggtag	agaataatcc	cacttctt	gcccgtcgat	gtgctccgat	300
attgatttgc	ctgggttggc	aagttagcgat	agcttctcc	aagtggaaaga	360
tcaagtgttc	gcggagcggt	aaacgatttgc	ttggctaagt	ggcatcaaga	420
gtcaataatg	tcccagctag	aatgcagtagt	gaaaaatca	cggtcacag	480
ctcaaggtca	agtttggttc	tgactttgaa	aagacaggga	attcttcttga	540
aactctgtcc	attcaggcga	aaagcagatt	cagattgtt	attttaagca	600
acagttagcg	tagatgtgt	taaaaatcca	ggagatgtgt	ttcaagatac	660
gaggatttaa	aacagagagg	aatttctgca	gagcgtcctt	ttcgagtgtt	720
gcttatgggc	gccaagtcta	tctcaagtttgc	gaaaccacga	gtaagagtga	780
gctgcttttgc	aagcttgc	aaaaggagtc	aaggtagctc	ctcagacaga	840
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gttgcacact	ttcaaaaatag	tacagactat	gtttagacta	agtttacagc	1080

ggagatttac tgctggatca tagtggtgcc tatgttgccc aatattatat tacttggaat	1140
gaatttatcct atgatcatca agttaaggaa gtcttactc ctaaggcttggacagaaat	1200
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gaaaaaaaccg atttgccact atgctgtaa cgacgattt ctatgggg aacaactctc	1380

<210> 11
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 <223> primer

<400> 11 gactaagctt gccaccatgg aaattaatgt gagtaaatta ag	42
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<210> 12
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 <212> DNA
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 <223> primer

<400> 12 ctgactcgag ttatTTTact gtaatcaagc catc	34
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<210> 13
 <211> 954
 <212> DNA
 <213> Artificial Sequence

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 <223> pSA-59 Aly insert

<400> 13 atgaaatatta atgtgagtaa attaagaaca gatttgccctc aagttggcgt gcaaccatattt agccaagtac acgcacactc aactggaaat ccgcattcaa ccgtacagaaa tgaagcggat tattcattggc gaaaaagaccc agaatttaggt tttttctcgc acattgttgg gaacggatgc atcatgcagg taggacctgt taataatggt gcctggacg ttggggcgg ttggaatgct gagacctatg cagcgggttga actgattgaa agccattcaa ctaaagaaga gttcatgacg gactaccgccc ttatatacgaa actcttacgc aatcttagcag atgaaggcagg tttggcggaaa acgcttgata cagggagttt agcttggaaattt aaaaacgcacg agtattgcac gaataaccaa ccaaaacaacc actcagacca tggatcca tacccttact tggcaaaatg gggcattagc cgtgagcagt ttaagcatga tattgagaac ggcttgacga ttggaaacagg ctggcagaag aatgacactg gctactggta cgtacattca gacggctt atccaaaaga caagttttag aaaaatcaatg gcacttggta ctactttgac agttcaggct atatgcttgc agaccgctgg aggaagcaca cagacggcaa ttggactac tttgaccaat caggcgaaat ggctacaggc ttggaaagaaaa tggctgagaa ttggactat ttcaacgaa aaggtggcat gaagacaggc ttggctcaagt acaaggacac ttggactac ttagacgcta aagaaggcgc aatggtatca aatgccttta tccagtcagc ggacggaaca ggctggact acctcaaacc agacggaaca ctggcagaca agccagaatt cacagtagag ccagatggct tgattacagt aaaa	60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 954
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<213> Artificial Sequence

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<223> polypeptide of pSA-59 Aly insert sequence

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	20					25							30		
Ser	Thr	Val	Gln	Asn	Glu	Ala	Asp	Tyr	His	Trp	Arg	Lys	Asp	Pro	Glu
	35				40						45				
Leu	Gly	Phe	Phe	Ser	His	Ile	Val	Gly	Asn	Gly	Cys	Ile	Met	Gln	Val
	50				55					60					
Gly	Pro	Val	Asn	Asn	Gly	Ala	Trp	Asp	Val	Gly	Gly	Gly	Trp	Asn	Ala
65		70					75						80		
Glu	Thr	Tyr	Ala	Ala	Val	Glu	Leu	Ile	Glu	Ser	His	Ser	Thr	Lys	Glu
	85					90						95			
Glu	Phe	Met	Thr	Asp	Tyr	Arg	Leu	Tyr	Ile	Glu	Leu	Leu	Arg	Asn	Leu
	100				105							110			
Ala	Asp	Glu	Ala	Gly	Leu	Pro	Lys	Thr	Leu	Asp	Thr	Gly	Ser	Leu	Ala
	115				120						125				
Gly	Ile	Lys	Thr	His	Glu	Tyr	Cys	Thr	Asn	Asn	Gln	Pro	Asn	Asn	His
	130				135						140				
Ser	Asp	His	Val	Asp	Pro	Tyr	Pro	Tyr	Leu	Ala	Lys	Trp	Gly	Ile	Ser
145					150					155			160		
Arg	Glu	Gln	Phe	Lys	His	Asp	Ile	Glu	Asn	Gly	Leu	Thr	Ile	Glu	Thr
	165					170					175				
Gly	Trp	Gln	Lys	Asn	Asp	Thr	Gly	Tyr	Trp	Tyr	Val	His	Ser	Asp	Gly
	180					185					190				
Ser	Tyr	Pro	Lys	Asp	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	
	195				200						205				
Phe	Asp	Ser	Ser	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr
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Asp	Gly	Asn	Trp	Tyr	Tyr	Phe	Asp	Gln	Ser	Gly	Glu	Met	Ala	Thr	Gly
225						230			235			240			
Trp	Lys	Lys	Ile	Ala	Glu	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Gly	Ala	
	245					250					255				
Met	Lys	Thr	Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp
	260					265					270				
Ala	Lys	Glu	Gly	Ala	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp
	275					280					285				
Gly	Thr	Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Lys
	290					295					300				
Pro	Glu	Phe	Thr	Val	Glu	Pro	Asp	Gly	Leu	Ile	Thr	Val	Lys		
305					310					315					

<210> 15

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> primer

<400> 15

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<210> 16
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<400> 16
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37

<210> 17
 <211> 1377
 <212> DNA
 <213> Artificial Sequence

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 cagaaaaaat atgatgagga tcagaagaaa actgaggcaa aagcggataa ggaagcaaaa 180
 gcatctgcgg aaatagataa agccacgtt gctgtacaaa gtgcgtatgt aaaattttta 240
 aatgtccaat ctaatcgta aatttcggag aatgaacgaa aaaaacaatt agcagaaata 300
 gataaagaga tagagaatgc taaacaaaaat ttacagaata aacaggaaga atttaataag 360
 gtttagagcag aagtaattcc tgaagcaaag gggtagctg ttactaaaca aaaagcggaa 420
 gaagctaaaa aagaagcaga agtagctaag agaaaatatg attatgcaac tctaaaggta 480
 gcactagcga agaaaagaatg agaggctaag gaacttggaa ttgaaaaact tcaatatgaa 540
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 gaaggcttag ataaagctct tactgataaa aaagtgtatgaa taaataatac tcaaaaaagca 1320
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 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide of pSA-60 PspA insert sequence

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35	40	45
Lys Lys Thr Glu Ala Lys Ala Asp Lys Glu Ala Lys Ala Ser Ala Glu		
50	55	60
Ile Asp Lys Ala Thr Phe Ala Val Gln Ser Ala Tyr Val Lys Phe Leu		
65	70	75
Asn Val Gln Ser Asn Arg Gln Ile Ser Glu Asn Glu Arg Lys Lys Gln		
85	90	95
Leu Ala Glu Ile Asp Lys Glu Ile Glu Asn Ala Lys Gln Asn Leu Gln		
100	105	110
Asn Lys Gln Glu Glu Phe Asn Lys Val Arg Ala Glu Val Ile Pro Glu		
115	120	125
Ala Lys Gly Leu Ala Val Thr Lys Gln Lys Ala Glu Glu Ala Lys Lys		
130	135	140
Glu Ala Glu Val Ala Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys Val		
145	150	155
160		
Ala Leu Ala Lys Lys Glu Val Glu Ala Lys Glu Leu Glu Ile Glu Lys		
165	170	175
Leu Gln Tyr Glu Ile Ser Thr Leu Glu Gln Glu Val Ala Ile Ala Gln		
180	185	190
His Gln Val Asp Asn Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro Asp		
195	200	205
Asp Gly Thr Lys Val Ile Glu Ala Lys Leu Asn Lys Gly Glu Ala Glu		
210	215	220
Leu Asn Ala Lys Gln Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu Glu		
225	230	235
240		
Lys Leu Leu Asp Ser Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu Leu		
245	250	255
Asp Lys Glu Ala Ala Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu Leu		
260	265	270
Gln Asn Lys Val Ala Asp Leu Glu Lys Gly Ile Ala Pro Tyr Gln Ile		
275	280	285
Lys Val Ala Glu Leu Asn Lys Glu Ile Ala Arg Leu Gln Ser Asp Leu		
290	295	300
Lys Asp Ala Glu Glu Asn Asn Val Glu Asp Tyr Ile Lys Glu Gly Leu		
305	310	315
320		
Glu Gln Ala Ile Ala Asp Lys Lys Ala Glu Leu Ala Thr Thr Gln Gln		
325	330	335
Asn Ile Asp Lys Thr Gln Lys Asp Leu Glu Asp Ala Glu Leu Glu Leu		
340	345	350
Glu Lys Val Leu Ala Thr Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu		
355	360	365
Leu Asp Lys Glu Ala Ala Glu Asp Ala Asn Ile Glu Ala Leu Gln Asn		
370	375	380
Lys Val Ala Asp Leu Glu Asn Lys Val Ala Glu Leu Asp Lys Glu Val		
385	390	395
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Thr Arg Leu Gln Ser Asp Leu Lys Asp Ala Glu Glu Asn Asn Val Glu		
405	410	415
Asp Tyr Val Lys Glu Gly Leu Asp Lys Ala Leu Thr Asp Lys Lys Val		
420	425	430
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Asp Thr Ala Leu Asn Glu Leu Gly Pro Asp Gly		
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<220>
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<210> 21
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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

<400> 23
Glu Asp Lys Val Glu Asn Asp
 1           5

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<213> Streptococcus pneumoniae

<400> 24
Tyr Pro Gln Val Glu Asp Lys Val Glu Asn Asp

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